

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 19, 2004, 01:14:52 / Search time 7.02288 Seconds

(without alignments)  
1468.042 Million cell updates/sec

Title: US-10-691-383-2\_COPY\_435\_632

Perfect score: 1039  
Sequence: 1 VNFQTSHYFRLLGAELAQR.....GLLGGTTTTLHQLMTF 198

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database: SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	* Query Match Length	ID	Description
1	93.5	90.0	557 1	PRXY_ASCNO
2	85.5	8.2	609 1	PRXC_CURIN
3	85.5	8.2	1819 1	GCPC_HUMAN
4	82.5	7.9	3370 1	Y374_METJA
5	82	7.9	857 1	RST2_SCHPO
6	79.5	7.7	158 1	YB0G_ECOLI
7	79.5	7.7	419 1	MUA2_STRPY
8	79.5	7.7	922 1	UB23_HUMAN
9	79.5	7.6	206 1	Y236_THBAC
10	78.5	7.6	454 1	SR54_AQUAE
11	77.5	7.5	940 1	PTGA_MYCPN
12	77.5	7.4	495 1	TOLC_ECOLI
13	76	7.3	394 1	PGK_BACME
14	75.5	7.3	426 1	APBB_MYCLE
15	75.5	7.3	493 1	GALT_LACTC
16	75.5	7.2	337 1	GLX_XYLEPT
17	75	7.2	774 1	STP_LAMBD
18	75	7.2	260 1	OPRI_NEIMC
19	74.5	7.2	835 1	VIRL_AERTU
20	74.5	7.1	237 1	YE1U_ECOLI
21	74	7.1	611 1	GLMS_PALSO
22	74	7.1	154 1	FMN_MORNO
23	73.5	7.1	472 1	GCSE_THREVO
24	73.5	7.1	803 1	DCML_HNDPS
25	73.5	7.0	603 1	LEPA_STY13
26	73	7.0	1163 1	Y222_HUMAN
27	73	7.0	216 1	Y007_TREBP
28	72.5	7.0	304 1	STKG_MOUSE
29	72.5	7.0	316 1	ARCC_BACLI
30	72.5	7.0	398 1	A23D_DROME
31	72.5	7.0	417 1	SAHH_MERTH
32	72.5	7.0	630 1	GIDA_PSEPU
33	72.5	7.0		

34	72.5	7.0	631 1	GIDA_PSEPK	Q88708 pseudomonas
35	72	6.9	337 1	GLK_XYLEFA	Q99204 xylella fas
36	72	6.9	488 1	GCSE_LYSIN	Q92C04 listeria in
37	72	6.9	527 1	PRCK_BACDI	Q9X707 bacillus ha
38	72	6.9	857 1	GELA_DICDI	P13466 dictyostel
39	71.5	6.9	466 1	STHA_YERPE	Q82497 yersinia pe
40	71.5	6.9	499 1	UDPG_YEAST	P32861 saccharomyc
41	71.5	6.9	555 1	LEUI_BRUME	Q8Y113 bruceella me
42	71.5	6.9	615 1	MUTA_MYCTU	P71773 mycobacteri
43	71.5	6.9	650 1	FLR2_HUMAN	O43155 homo sapien
44	71.5	6.9	878 1	ACON_PICCN	Q92990 rickettsia
45	71	6.8	222 1	TOXK_PICFA	P19972 p salt-nedi

## ALIGNMENTS

RESULT 1	PRXY_ASCNO	STANDARD;	PRT;	557 AA.
ID	PRXY_ASCNO			
AC	P81701;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Vanadium haloperoxidase (EC 1.11.1.-) (V-BPO).			
OS	Ascopyllum nodosum (Knotted wrack) (Brown seaweed).			
OC	Eukaryota; Stramenopiles; Phaeophyceae; Fucales; Fucaceae;			
OC	Ascopyllum.			
OX	NCBI_TaxID=52969;			
RN	[1]			
RP	SEQUENCE, X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS), AND FUNCTION.			
RX	MEDLINE=20013071; PubMed=10543953;			
RA	Weyand M., Hecht H.-U., Kiess M., Llaud M.-F., Valtter H.,			
RA	Schomburg D.;			
RT	"X-ray structure determination of a vanadium-dependent			
RT	haloperoxidase from Ascopyllum nodosum at 2.0-A resolution."			
RL	J. Mol. Biol. 293:595-611(1999).			
RN	[2]			
RP	SEQUENCE OF 326-556 FROM N.A., SEQUENCE OF 326-341; 383-426; 471-479			
RP	AND 481-556, AND FUNCTION			
RX	MEDLINE=96081028; PubMed=8564812;			
RA	Valter H.;			
RA	"Vanadium-dependent haloperoxidases.";			
RL	(In) Sigel H., Sigel A. (eds.);			
RL	Metal ions in biological system-vanadium and its role in life,			
RL	pp.31:325-362, Marcel Dekker, New York (1995).			
CC	-1- CATALYTIC ACTIVITY: Halide + H(2)O(2) + H(+) = HOHal + H(2)O.			
CC	-1- SUBUNIT: Homodimer; disulfide-linked.			
CC	-1- SIMILARITY: TO OTHER BACTERIAL NON-HEME BROMO- AND CHLORO-			
CC	PEROXIDASES.			
DR	PDB: 1OI9; 10-JUN-00.			
DR	InterPro: IPR008934; AcPage VanPerase.			
DR	InterPro: IPR00126; Pf_PPase.			
KW	Oxidoreductase; Peroxidase; Vanadium; 3D-structure;			
KW	Pyrolydione carboxylic acid.			
KW	MOD RES			
FT	DISULFID	1	3	3
FT	DISULFID	41	41	41
FT	DISULFID	77	77	86
FT	DISULFID	441	462	
FT	DISULFID	544	555	
FT	ACT SITE	411	411	
FT	ACT SITE	418	418	
FT	METAL	486	486	
FT	CONFLICT	321	321	
FT	CONFLICT	341	341	
FT	CONFLICT	403	404	
FT	CONFLICT	407	408	
FT	CONFLICT	409	409	
FT	CONFLICT	441	444	
FT	CONFLICT	470	470	
FT	HELEX	15	37	



T HELIX 50 52  
 T STRAND 53 53  
 T TURN 56 57  
 T STRAND 57 57  
 T TURN 60 60  
 T STRAND 62 62  
 T TURN 66 66  
 T STRAND 68 80  
 T HELIX 83 87  
 T TURN 88 88  
 T HELIX 98 100  
 T STRAND 102 103  
 T TURN 105 108  
 T TURN 118 119  
 T TURN 129 130  
 T HELIX 132 146  
 T TURN 147 149  
 T HELIX 152 154  
 T TURN 155 157  
 T HELIX 159 170  
 T TURN 172 173  
 T HELIX 174 176  
 T TURN 178 179  
 T STRAND 180 180  
 T TURN 184 185  
 T TURN 190 195  
 T STRAND 197 197  
 T TURN 200 203  
 T HELIX 210 213  
 T STRAND 216 218  
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 T STRAND 221 223  
 T STRAND 227 227  
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 T STRAND 455 457  
 T TURN 464 464  
 T HELIX 465 483  
 T TURN 484 484  
 T HELIX 488 512  
 T STRAND 522 522  
 T TURN 519 525

FT STRAND 528 531  
 FT TURN 533 534  
 FT STRAND 537 539  
 FT TURN 540 541  
 FT STRAND 542 543  
 FT TURN 552 554  
 SQ SEQUENCE 557 AA; 60343 MW; E3D8557AB92B16F4 CRC64;  
 Query Match 90.0%; Score 935; DB 1; Length 557;  
 Best Local Similarity 89.4%; Pred. No. 6,9e-81;  
 Matches 177; Conservative 12; Mismatches 9; Indels 0; Gaps 0;  
 QY 1 VNFQSHYFRLIGAAELAGACSCYQKQVHRPAREALGGTLANTIADLDADPDISILE 60  
 DB 316 VNFQSHYFRLIGAAELAGACSCYQKQVHRPAREALGGTLANTIADLDADPDISILE 375  
 QY 61 NDELLKRVAINAQNPNNEVTYLLPOALQVGSPTHPSPSGHATONGAFATYVKALIGL 120  
 DB 376 NAEELKRVAINAQNPNNEVTYLLPOALQVGSPTHPSPSGHATONGAFATYVKALIGL 435  
 QY 121 DRGECFPPNPVPSDDGLINFBGACLTGEGEINKAVNVAFGROMLGIHYRFDGIQGL 180  
 DB 436 DRGDCYPPNPVPSDDGLINFBGACLTGEGEINKAVNVAFGROMLGIHYRFDGIQGL 495  
 QY 181 LIGETITVRLHQLMTF 198  
 DB 496 LIGETITVRLHQLMTF 513  
 RESULT 2  
 ID PRXC\_CURIN STANDARD; PRT: 609 AA.  
 AC P49053;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Vanadium chloroperoxidase (EC 1.11.1.10) (VCPO) (Vanadium chloride peroxidase).  
 GN CPO.  
 OS Curvularia inaequalis.  
 CC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;  
 CC Pleosporales; Pleosporaceae; Cochliophiales.  
 CC NCB1\_taxid=38902;  
 RX MEDLINE=95262722; PubMed=7744081;  
 RA Simons B.H., Barnett P., Vollenbroek E.G.M., Dekker H.L.,  
 RA Mijsters A.O., Messerschmidt A., Meyer R.;  
 RT "Primary structure and characterization of the vanadium  
 RT chloroperoxidase from the fungus Curvularia inaequalis";  
 RL Eur. J. Biochem. 229:566-574(1995).  
 RN [2]  
 RN X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).  
 RX MEDLINE=96133943; PubMed=8552646;  
 RA Messerschmidt A., Meyer R.;  
 RT "X-ray structure of a vanadium-containing enzyme: chloroperoxidase  
 RT from the fungus Curvularia inaequalis";  
 RL Proc. Natl. Acad. Sci. U.S.A. 93:392-396(1996).  
 CC -1- CATALYTIC ACTIVITY: 2 RH + 2 chloride + H(2)O(2) = 2 RCl + 2  
 CC H(2)O.  
 CC -1- COFACTOR: Vanadium.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- PTM: The N-terminus is blocked.  
 CC -----  
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 CC -----  
 DR EMBL: X85369; CAA59686.1; -